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SEQUENCE LISTING

<110> BECKMANN, JACQUES
RICHARD, ISABELLE

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Asp Gln Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn
            740                 745                 750

Asp Ala Gly Phe His Leu Asn Asn Gln Leu Tyr Asp Ile Ile Thr Met
        755                 760                 765

Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys
    770                 775                 780

Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp
785                 790                 795                 800
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Lys Asp Gly Asp Gly Ile Ile Lys Leu Asn Val Leu Glu Trp Leu Gln
                805                 810                 815

Leu Thr Met Tyr Ala
            820

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Met Pro Thr Val Ile Ser Pro Thr Val Ala Pro Arg Thr Gly Ala Glu
  1               5                  10                  15

Pro Arg Ser Pro Gly Pro Val Pro His Pro Ala Gln Gly Lys Thr Thr
            20                  25                  30

Glu Ala Gly Gly Gly His Pro Gly Gly Ile Tyr Ser Ala Ile Ile Ser
        35                  40                  45

Arg Asn Phe Pro Ile Ile Gly Val Lys Glu Lys Thr Phe Glu Gln Leu
    50                  55                  60
```

```
His Lys Lys Cys Leu Glu Lys Lys Val Leu Tyr Leu Asp Pro Glu Phe
 65                  70                  75                  80

Pro Pro Asp Glu Thr Ser Leu Phe Tyr Ser Gln Lys Phe Pro Ile Gln
                85                  90                  95

Phe Val Trp Lys Arg Pro Pro Glu Ile Cys Glu Asn Pro Arg Phe Ile
            100                 105                 110

Ile Gly Gly Ala Asn Arg Thr Asp Ile Cys Gln Gly Asp Leu Gly Asp
        115                 120                 125

Cys Trp Leu Leu Ala Ala Ile Ala Cys Leu Thr Leu Asn Glu Arg Leu
    130                 135                 140

Leu Phe Arg Val Ile Pro His Asp Gln Ser Phe Thr Glu Asn Tyr Ala
145                 150                 155                 160

Gly Ile Phe His Phe Gln Phe Trp Arg Tyr Gly Asp Trp Val Asp Val
                165                 170                 175

Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr
            180                 185                 190

Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala
        195                 200                 205

Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr
    210                 215                 220

Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Thr Glu Phe Phe Glu
225                 230                 235                 240

Ile Lys Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Arg Lys Ala Ile
                245                 250                 255

Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met
            260                 265                 270

Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Glu Leu Ile Ala
        275                 280                 285

Arg Met Val Arg Asn Met Asp Asn Ser Leu Leu Arg Asp Ser Asp Leu
    290                 295                 300

Asp Pro Arg Ala Ser Asp Asp Arg Pro Ser Arg Thr Ile Val Pro Val
305                 310                 315                 320

Gln Tyr Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr
                325                 330                 335

Ser Val Thr Gly Leu Glu Glu Ala Leu Phe Lys Gly Glu Lys Val Lys
            340                 345                 350

Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser
        355                 360                 365

Trp Ser Asp Gly Trp Lys Asp Trp Ser Phe Val Asp Lys Asp Glu Lys
    370                 375                 380
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Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser
385 390 395 400

Tyr Asp Asp Phe Val Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu
405 410 415

Thr Ala Asp Ala Leu Glu Ser Asp Lys Leu Gln Thr Trp Thr Val Ser
420 425 430

Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Gly Cys Arg
435 440 445

Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu
450 455 460

Leu Glu Glu Asp Asp Asp Pro Asp Asp Ser Glu Val Ile Cys Ser Phe
465 470 475 480

Leu Val Ala Leu Met Gln Lys Asn Arg Arg Lys Asp Arg Lys Leu Gly
485 490 495

Ala Asn Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu
500 505 510

Met His Gly Asn Lys Gln His Leu Gln Lys Asp Phe Phe Leu Tyr Asn
515 520 525

Ala Ser Lys Ala Arg Ser Lys Thr Tyr Ile Asn Met Arg Glu Val Ser
530 535 540

Gln Arg Phe Arg Leu Pro Pro Ser Glu Tyr Val Ile Val Pro Ser Thr
545 550 555 560

Tyr Glu Pro His Gln Glu Gly Glu Phe Ile Leu Arg Val Phe Ser Glu
565 570 575

Lys Arg Asn Leu Ser Glu Glu Ala Glu Asn Thr Ile Ser Val Asp Arg
580 585 590

Pro Val Lys Lys Lys Lys Asn Lys Pro Ile Ile Phe Val Ser Asp Arg
595 600 605

Ala Asn Ser Asn Lys Glu Leu Gly Val Asp Gln Glu Ala Glu Glu Gly
610 615 620

Lys Asp Lys Thr Gly Pro Asp Lys Gln Gly Glu Ser Pro Gln Pro Arg
625 630 635 640

Pro Gly His Thr Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn
645 650 655

Ile Phe Arg Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu
660 665 670

Leu Lys Asn Val Leu Asn Thr Val Val Asn Lys His Lys Asp Leu Lys
675 680 685

Thr Gln Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met
690 695 700

Asp Thr Asp Gly Ser Gly Arg Leu Asn Leu Gln Glu Phe His His Leu

705 710 715 720

Trp Lys Lys Ile Lys Ala Trp Gln Lys Ile Phe Lys His Tyr Asp Thr
725 730 735

Asp His Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn
740 745 750

Asp Ala Gly Phe His Leu Asn Ser Gln Leu Tyr Asp Ile Ile Thr Met
755 760 765

Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys
770 775 780

Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp
785 790 795 800

Lys Asp Gly Asp Gly Ile Ile Lys Leu Asn Val Leu Glu Trp Leu Gln
805 810 815

Leu Thr Met Tyr Ala
820

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Met Pro Thr Val Ile Ser Ala Ser Val Ala Pro Arg Thr Ala Ala Glu
 1               5                  10                  15

Pro Arg Ser Pro Gly Pro Val Pro His Pro Ala Gln Ser Lys Ala Thr
            20                  25                  30

Glu Ala Gly Gly Gly Asn Pro Ser Gly Ile Tyr Ser Ala Ile Ile Ser
        35                  40                  45

Arg Asn Phe Pro Ile Ile Gly Val Lys Glu Lys Thr Phe Glu Gln Leu
    50                  55                  60

His Lys Lys Cys Leu Glu Lys Lys Val Leu Tyr Val Asp Pro Glu Phe
65                  70                  75                  80

Pro Pro Asp Glu Thr Ser Leu Phe Tyr Ser Gln Lys Phe Pro Ile Gln
                85                  90                  95

Phe Val Trp Lys Arg Pro Pro Glu Ile Cys Glu Asn Pro Arg Phe Ile
            100                 105                 110

Ile Asp Gly Ala Asn Arg Thr Asp Ile Cys Gln Gly Glu Leu Gly Asp
        115                 120                 125

Cys Trp Phe Leu Ala Ala Ile Ala Cys Leu Thr Leu Asn Gln His Leu
    130                 135                 140

Leu Phe Arg Val Ile Pro His Asp Gln Ser Phe Ile Glu Asn Tyr Ala
145                 150                 155                 160

Gly Ile Phe His Phe Gln Phe Trp Arg Tyr Gly Glu Trp Val Asp Val
                165                 170                 175

Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr
            180                 185                 190

Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala
        195                 200                 205

Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr
    210                 215                 220

Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Ala Glu Phe Phe Glu
225                 230                 235                 240

Ile Arg Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Lys Lys Ala Ile
                245                 250                 255

Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met
            260                 265                 270

Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Asp Leu Ile Ala
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275 280 285

Arg Met Val Arg Asn Met Glu Asn Ser Arg Leu Arg Asp Ser Ile Leu
290 295 300

Asp Pro Glu Val Ser Asp Asp Arg Pro Thr Arg Thr Ile Val Pro Val
305 310 315 320

Gln Phe Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr
325 330 335

Ser Val Thr Gly Leu Glu Glu Ala Leu Phe Lys Gly Glu Lys Val Lys
340 345 350

Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser
355 360 365

Trp Ser Asp Ser Trp Lys Asp Trp Ser Phe Val Asp Lys Asp Glu Lys
370 375 380

Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser
385 390 395 400

Tyr Asp Asp Phe Ile Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu
405 410 415

Thr Ala Asp Ala Leu Glu Ser Asp Lys Leu Gln Thr Trp Thr Val Ser
420 425 430

Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Thr Gly Arg
435 440 445

Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu
450 455 460

Leu Glu Glu Asp Asp Asp Pro Asp Asp Ser Glu Val Ile Cys Ser Phe
465 470 475 480

Leu Val Ala Leu Met Gln Arg Asn Arg Arg Lys Asp Arg Lys Leu Gly
485 490 495

Ala Asn Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu
500 505 510

Met His Gly Asn Lys Gln His Leu Gln Lys Asp Phe Phe Leu Tyr Asn
515 520 525

Ala Ser Lys Ala Arg Ser Arg Thr Tyr Ile Asn Met Arg Glu Val Ser
530 535 540

Glu Arg Phe Arg Leu Pro Pro Ser Glu Tyr Val Ile Val Pro Ser Thr
545 550 555 560

Tyr Glu Pro His Gln Glu Gly Glu Phe Met Leu Arg Val Phe Ser Glu
565 570 575

Lys Arg Lys Leu Ser Glu Glu Val Glu Asn Thr Ile Ser Val Asp Arg
580 585 590

Pro Val Arg Lys Lys Lys Thr Lys Pro Ile Ile Phe Val Ser Asp Arg
595 600 605

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Ala Asn Ser Asn Lys Glu Leu Gly Val Asp Gln Glu Ser Glu Glu Gly
    610                 615                 620

Gln Asp Lys Thr Ser Pro Asp Lys Gln Glu Lys Ser Pro Lys Pro Glu
625                 630                 635                 640

Pro Ser Asn Thr Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn
                645                 650                 655

Ile Phe Lys Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu
            660                 665                 670

Leu Lys Lys Val Leu Asn Thr Val Val Asn Lys His Lys Asp Leu Lys
        675                 680                 685

Thr His Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met
    690                 695                 700

Asp Thr Asp Gly Ser Gly Lys Leu Asn Leu Gln Glu Phe His His Leu
705                 710                 715                 720

Trp Asn Lys Ile Lys Ala Trp Gln Lys Ile Phe Lys His Tyr Asp Thr
                725                 730                 735

Asp Gln Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn
            740                 745                 750

Asp Ala Gly Phe His Leu Asn Asn Gln Leu Tyr Asp Ile Ile Thr Met
        755                 760                 765

Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys
    770                 775                 780

Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp
785                 790                 795                 800

Lys Asp Gly Asp Gly Ile Ile Lys Leu Asn Val Leu Glu Trp Leu Gln
                805                 810                 815

Leu Thr Met Tyr Ala
            820
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Met Pro Thr Val Ile Ser Ala Ser Val Ala Pro Arg Thr Ala Ala Glu
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Pro Arg Ser Pro Gly Pro Val Pro His Pro Ala Gln Ser Lys Ala Thr
             20                  25                  30

Glu Ala Gly Gly Gly Asn Pro Ser Gly Ile Tyr Ser Ala Ile Ile Ser
         35                  40                  45

Arg Asn Phe Pro Ile Ile Gly Val Lys Glu Lys Thr Phe Glu Gln Leu
     50                  55                  60

His Lys Lys Cys Leu Glu Lys Lys Val Leu Tyr Val Asp Pro Glu Phe
 65                  70                  75                  80

Pro Pro Asp Glu Thr Ser Leu Phe Tyr Ser Gln Lys Phe Pro Ile Gln
                 85                  90                  95

Phe Val Trp Lys Arg Pro Pro Glu Ile Cys Glu Asn Pro Arg Phe Ile
            100                 105                 110

Ile Asp Gly Ala Asn Arg Thr Asp Ile Cys Gln Gly Glu Leu Gly Asp
        115                 120                 125

Cys Trp Phe Leu Ala Ala Ile Ala Cys Leu Thr Leu Asn Gln His Leu
    130                 135                 140

Leu Phe Arg Val Ile Pro His Asp Gln Ser Phe Ile Glu Asn Tyr Ala
145                 150                 155                 160

Gly Ile Phe His Phe Gln Phe Trp Arg Tyr Gly Glu Trp Val Asp Val
                165                 170                 175
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Val Ile Asp Asp Cys Leu Pro Thr Tyr Asn Asn Gln Leu Val Phe Thr
180 185 190

Lys Ser Asn His Arg Asn Glu Phe Trp Ser Ala Leu Leu Glu Lys Ala
195 200 205

Tyr Ala Lys Leu His Gly Ser Tyr Glu Ala Leu Lys Gly Gly Asn Thr
210 215 220

Thr Glu Ala Met Glu Asp Phe Thr Gly Gly Val Ala Glu Phe Phe Glu
225 230 235 240

Ile Arg Asp Ala Pro Ser Asp Met Tyr Lys Ile Met Lys Lys Ala Ile
245 250 255

Glu Arg Gly Ser Leu Met Gly Cys Ser Ile Asp Asp Gly Thr Asn Met
260 265 270

Thr Tyr Gly Thr Ser Pro Ser Gly Leu Asn Met Gly Glu Leu Ile Glu
275 280 285

Arg Met Val Arg Asn Met Asp Asn Ser Arg Leu Arg Asp Ser Ile Leu
290 295 300

Asp Pro Glu Val Ser Asp Asp Arg Pro Thr Arg Met Ile Val Pro Val
305 310 315 320

Gln Phe Glu Thr Arg Met Ala Cys Gly Leu Val Arg Gly His Ala Tyr
325 330 335

Ser Val Thr Gly Leu Glu Glu Ala Leu Tyr Lys Gly Glu Lys Val Lys
340 345 350

Leu Val Arg Leu Arg Asn Pro Trp Gly Gln Val Glu Trp Asn Gly Ser
355 360 365

Trp Ser Asp Ser Trp Lys Asp Trp Ser Tyr Val Asp Lys Asp Glu Lys
370 375 380

Ala Arg Leu Gln His Gln Val Thr Glu Asp Gly Glu Phe Trp Met Ser
385 390 395 400

Tyr Glu Asp Phe Ile Tyr His Phe Thr Lys Leu Glu Ile Cys Asn Leu
405 410 415

Thr Ala Asp Ala Leu Gln Ser Asp Lys Leu Gln Thr Trp Thr Val Ser
420 425 430

Val Asn Glu Gly Arg Trp Val Arg Gly Cys Ser Ala Gly Gly Cys Arg
435 440 445

Asn Phe Pro Asp Thr Phe Trp Thr Asn Pro Gln Tyr Arg Leu Lys Leu
450 455 460

Leu Glu Glu Asp Asp Asp Pro Asp Asp Ser Glu Val Ile Cys Ser Phe
465 470 475 480

Leu Val Ala Leu Met Gln Lys Asn Arg Arg Lys Asp Arg Lys Leu Gly
485 490 495

Ala Ser Leu Phe Thr Ile Gly Phe Ala Ile Tyr Glu Val Pro Lys Glu
500 505 510

Met His Gly Asn Lys Gln His Leu Gln Lys Asp Phe Phe Leu Tyr Asn
515 520 525

Ala Ser Lys Ala Arg Ser Lys Thr Tyr Ile Asn Met Arg Glu Val Ser
530 535 540

Gln Arg Phe Arg Leu Pro Pro Ser Glu Tyr Val Ile Val Pro Ser Thr
545 550 555 560

Tyr Glu Pro His Gln Glu Gly Glu Phe Ile Leu Arg Val Phe Ser Glu
565 570 575

Lys Arg Asn Leu Ser Glu Glu Val Glu Asn Thr Ile Ser Val Asp Arg
580 585 590

Pro Val Lys Lys Lys Lys Thr Lys Pro Ile Ile Phe Val Ser Asp Arg
595 600 605

Ala Asn Ser Asn Lys Glu Leu Gly Val Asp Gln Glu Ser Glu Glu Gly
610 615 620

Lys Gly Lys Thr Ser Pro Asp Lys Gln Lys Gln Ser Pro Gln Pro Gln
625 630 635 640

Pro Gly Ser Ser Asp Gln Glu Ser Glu Glu Gln Gln Gln Phe Arg Asn
645 650 655

Ile Phe Lys Gln Ile Ala Gly Asp Asp Met Glu Ile Cys Ala Asp Glu
660 665 670

Leu Lys Lys Val Leu Asn Thr Val Val Asn Lys His Lys Asp Leu Lys
675 680 685

Thr His Gly Phe Thr Leu Glu Ser Cys Arg Ser Met Ile Ala Leu Met
690 695 700

Asp Thr Asp Gly Ser Gly Lys Leu Asn Leu Gln Glu Phe His His Leu
705 710 715 720

Trp Asn Lys Ile Lys Ala Trp Gln Lys Ile Phe Lys His Tyr Asp Thr
725 730 735

Asp Gln Ser Gly Thr Ile Asn Ser Tyr Glu Met Arg Asn Ala Val Asn
740 745 750

Asp Ala Gly Phe His Leu Asn Asn Gln Leu Tyr Asp Ile Ile Thr Met
755 760 765

Arg Tyr Ala Asp Lys His Met Asn Ile Asp Phe Asp Ser Phe Ile Cys
770 775 780

Cys Phe Val Arg Leu Glu Gly Met Phe Arg Ala Phe His Ala Phe Asp
785 790 795 800

Lys Asp Gly Asp Gly Ile Ile Lys Leu Asn Val Leu Glu Trp Leu Gln
805 810 815

Leu Thr Met Tyr Ala

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<210> 17
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<210> 33
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<212> DNA
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<212> DNA
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<212> DNA
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<210> 43
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<210> 45
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ttcaacctct ggagtgggcc 20

<210> 46
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caccagagca aaccgtccac 20

<210> 47
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<212> DNA
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acagcccaga ctcccattcc 20

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<400> 48
ttctcttctc ccttcaccct 20

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<220>
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<400> 49
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<210> 50
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<220>
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<220>
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gacaaactcc tgggaagcct 20

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acctctgacc cctgtgaacc 20

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<220>
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<400> 57
accctgtatg ttgccttgg 19

<210> 58
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<210> 59
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attcctgctc ccaccgtctc 20

<210> 60
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<210> 61
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<212> DNA
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<400> 61
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<210> 62
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<400> 62
cagagtgtcc gagaggcagg g 21

<210> 63
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cgttgacccc tccaccttga 20

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<400> 65

taggggtaa aatggaggag 20

<210> 66
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<400> 66
actaactcag tggaataggg 20

<210> 67
<211> 19
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<400> 67
ggagctagga tagctcaat 19

<210> 68
<211> 1302
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(1302)
<223> /note= Flanking 5' genomic region of the sequence of the human nCL1 cDNA described in Figure 2a

<220>
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<222> (-477)..(-472)
<223> /note= Putative Sp1 in Figure 2a

<220>
<221> misc_feature
<222> (-364)..(-343)
<223> /note= MEF2 binding sites in Figure 2a

<220>
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<222> (-685)..(-672)
<223> /note= CArG box in Figure 2a

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ttaagacgga gtctctttct gtcacctggg ctggagtgca gtggcgtgat ctgggttcac 180
tacaacctct ccctcctggg ttcaagcaat tcttctgtct cagcctccca agtagctggg 240
attacaggca ccccccgcca cacccggctt atttttgtat ttttagtaga gacagggttt 300
cactattgtt gtccatgctg gtctcgaact cgtgacctca tgtgatccac ccgcctcggc 360

ctcccaaagt gcagagatta gagacgtgat ccacatggcc cagcaggacc acttttagc 420
agattcagtc ccagtgttca ttttgtggat ggggagagac aagaggtggc aaggtcaagt 480
gtgcaggtag agacagggat tttctcaaat gaggactctg ctgagtagca ttttccatgc 540
agacatttcc aatgagcgct gacccaagaa cattctaaaa aagataccaa atctaacatt 600
gaataatgtt ctgatatcct aaaattttag gactaaaaat catgttctct aaaattcaca 660
gaatattttt gtagaattca gtacctcccg ttcaccctaa ctagcttttt tgcaatattg 720
ttttccattc atttgatggc cagtagttgg gtggtctgta taactgccta ctcaataaca 780
tgtcagcagt tctcagcttc tttccagtgt tcaccttact cagatactcc cttttcattt 840
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tgacagaatt actccaactt ccccctttgca gttgcttcct ttccttgaag gtagctgtat 1260
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<210> 69
<211> 1381
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1381)
<223> /note= Flanking 3' genomic region of the sequence of the human nCL1 cDNA described in Figure 2c

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tttacctcaa aggacccagc agctacaccc ctacaggctt ccaggcacct catcagtcat 132
gttcctcctc cattttaccc cctacccatc cttgatcggt catgcctagc ctgacccttt 192
agtaaagcaa tgaggtagga agaacaaacc cttgtccctt tgccatgtgg aggaaagtgc 252
ctgcctctgg tccgagccgc ctcggttctg aagcgagtgc tcctgcttac cttgctctag 312
gctgtctgca gaagcacctg ccggtggcac tcagcacctc cttgtgctag agccctccat 372
caccttcacg ctgtcccacc atgggccagg aaccaaacca gcactgggtt ctactgctgt 432
ggggtaaact aactcagtgg aatagggctg gttactttgg gctgtccaac tcataagttt 492
ggctgcattt tgaaaaaagc tgatctaaat aaaggcatgt gtatggctgg tccccttgtg 552
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tcacctatca cctacaagag aacaatgaaa aacacacaca aaaacaaaat cttgaatttt 672
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